



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/759,130

Source: OIPE

Date Processed by STIC: 1-29-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/759,130

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213> Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220> Feature (NEW RULES) Sequence(s) _____ are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: MCCARTHY, Sean A
 4 FRASER, Christopher C
 5 SHARP, John D
 6 BARNES, Thomas S
 7 KIRST, Susan J
 8 MACKAY, Charles R
 9 MYERS, Paul S
 10 LEIBY, Kevin R
 11 WRIGHTON, Nicholas
 12 GOODEARL, Andrew
 13 HOLTZMAN, Douglas A
 15 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC,
 16 DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER USES
 18 <130> FILE REFERENCE: 210147.0066/66US
 C--> 20 <140> CURRENT APPLICATION NUMBER: US/09/759,130
 21 <141> CURRENT FILING DATE: 2001-01-12
 23 <150> PRIOR APPLICATION NUMBER: US 09/479,249
 24 <151> PRIOR FILING DATE: 2000-01-07
 26 <150> PRIOR APPLICATION NUMBER: US 09/559,497
 27 <151> PRIOR FILING DATE: 2000-04-27
 29 <150> PRIOR APPLICATION NUMBER: US 09/578,063
 30 <151> PRIOR FILING DATE: 2000-05-24
 32 <150> PRIOR APPLICATION NUMBER: US 09/333,159
 33 <151> PRIOR FILING DATE: 1999-06-14
 35 <150> PRIOR APPLICATION NUMBER: US 09/596,194
 36 <151> PRIOR FILING DATE: 2000-07-14
 38 <150> PRIOR APPLICATION NUMBER: US 09/342,364
 39 <151> PRIOR FILING DATE: 1999-06-29
 41 <150> PRIOR APPLICATION NUMBER: US 09/608,452
 42 <151> PRIOR FILING DATE: 2000-06-30
 44 <150> PRIOR APPLICATION NUMBER: US 09/393,996
 45 <151> PRIOR FILING DATE: 1999-09-10
 47 <150> PRIOR APPLICATION NUMBER: US 09/602,871
 48 <151> PRIOR FILING DATE: 2000-06-23
 50 <150> PRIOR APPLICATION NUMBER: US 09/420,707
 51 <151> PRIOR FILING DATE: 1999-10-19
 53 <160> NUMBER OF SEQ ID NOS: 460
 55 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

216 <210> SEQ ID NO: 3
 217 <211> LENGTH: 1151
 218 <212> TYPE: PRT
 219 <213> ORGANISM: Homo sapiens
 221 <400> SEQUENCE: 3

Number of amino acids differ:
 -1151 listed
 911 shown

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

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222 Met His Gln Met Asn Ala Lys Met His Phe Arg Phe Val Phe Ala Leu
223   1           5           10           15
225 Leu Ile Val Ser Phe Asn His Asp Val Leu Gly Lys Asn Leu Lys Tyr
226           20           25           30
228 Arg Ile Tyr Glu Glu Gln Arg Val Gly Ser Val Ile Ala Arg Leu Ser
229           35           40           45
231 Glu Asp Val Ala Asp Val Leu Leu Lys Leu Pro Asn Pro Ser Thr Val
232           50           55           60
234 Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro Leu Leu Val Val Asn
235   65           70           75           80
237 Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr Ile Asp Arg Glu Gln
238           85           90           95
240 Thr Leu Pro Thr Glu His Leu Gln Leu Phe His Ile Glu Val Glu Val
241           100          105          110
243 Leu Asp Ile Asn Asp Asn Ser Pro Gln Phe Ser Arg Ser Leu Ile Pro
244           115          120          125
246 Ile Glu Ile Ser Glu Ser Ala Ala Val Gly Thr Arg Ile Pro Leu Asp
247           130          135          140
249 Ser Ala Phe Asp Pro Asp Val Gly Glu Asn Ser Leu His Thr Tyr Ser
250 145           150          155          160
252 Leu Ser Ala Asn Asp Phe Phe Asn Ile Glu Val Arg Thr Arg Thr Asp
253           165          170          175
255 Glu Leu Lys Ser Ser Tyr Glu Leu Gln Leu Thr Ala Ser Asp Met Gly
256           180          185          190
258 Val Pro Gln Arg Ser Gly Ser Ser Ile Leu Lys Ile Ser Ile Ser Asp
259           195          200          205
261 Ser Asn Asp Asn Ser Pro Ala Phe Glu Gln Gln Ser Tyr Ile Ile Gln
262           210          215          220
264 Leu Leu Glu Asn Ser Pro Val Gly Thr Leu Leu Asp Leu Asn Ala
265 225           230          235          240
267 Thr Asp Pro Asp Glu Gly Ala Asn Gly Lys Ile Val Tyr Ser Phe Ser
268           245          250          255
270 Ser His Val Ser Pro Lys Ile Met Glu Thr Phe Lys Ile Asp Ser Glu
271           260          265          270
273 Lys Ser Tyr Glu Ile Asp Val Gln Ala Gln Asp Leu Gly Pro Asn Ser
274           275          280          285
276 Ile Pro Ala His Cys Lys Ile Ile Ile Lys Val Val Asp Val Asn Asp
277           290          295          300
279 Asn Lys Pro Glu Ile Asn Ile Asn Leu Met Ser Pro Gly Lys Glu Glu
280 305           310          315          320
282 Ile Ser Tyr Ile Phe Glu Gly Asp Pro Ile Asp Thr Phe Val Ala Leu
283           325          330          335
285 Val Arg Val Gln Asp Lys Asp Ser Gly Leu Asn Gly Glu Ile Val Cys
286           340          345          350
288 Asn Asn Tyr Leu Ile Leu Thr Asn Ala Thr Leu Asp Arg Glu Lys Arg
289           355          360          365
291 Ser Glu Tyr Ser Leu Thr Val Ile Ala Glu Asp Arg Gly Thr Pro Ser
292           370          375          380
294 Leu Ser Thr Val Lys His Phe Thr Val Gln Ile Asn Asp Ile Asn Asp

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Input Set : A:\10147-61.txt

Output Set: N:\CRF3\01292001\I759130.raw

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295 385          390          395          400
297 Asn Pro Pro His Phe Gln Arg Ser Arg Tyr Glu Phe Val Ile Ser Glu
298          405          410          415
300 Asn Asn Ser Pro Gly Ala Tyr Ile Thr Thr Val Thr Ala Thr Asp Pro
301          420          425          430
303 Phe Ile Leu Gly Ser Ser Ile Thr Thr Tyr Val Thr Ile Asp Pro Ser
304          435          440          445
306 Asn Gly Ala Ile Tyr Ala Leu Arg Ile Phe Asp His Glu Glu Val Ser
307          450          455          460
309 Gln Ile Thr Phe Val Val Glu Ala Arg Asp Gly Gly Ser Pro Lys Gln
310 465          470          475          480
312 Leu Val Ser Asn Thr Thr Val Val Leu Thr Ile Ile Asp Glu Asn Asp
313          485          490          495
315 Asn Val Pro Val Val Ile Gly Pro Ala Leu Arg Asn Asn Thr Ala Glu
316          500          505          510
318 Ile Thr Ile Pro Lys Gly Ala Glu Ser Gly Phe His Val Thr Arg Ile
319          515          520          525
321 Ala Ile Val Ala Gly Asn Glu Glu Asn Ile Phe Ile Ile Asp Pro Arg
322          530          535          540
324 Ser Cys Asp Ile His Thr Asn Val Ser Met Asp Ser Val Pro Tyr Thr
325 545          550          555          560
327 Glu Trp Glu Leu Ser Val Ile Ile Gln Asp Lys Gly Asn Pro Gln Leu
328          565          570          575
330 His Thr Lys Val Leu Leu Lys Cys Met Ile Phe Glu Tyr Ala Glu Ser
331          580          585          590
333 Val Thr Ser Thr Ala Met Thr Ser Val Ser Gln Ala Ser Leu Asp Val
334          595          600          605
336 Leu Val Ile Met Val Leu Phe Ala Thr Arg Cys Asn Arg Glu Lys Lys
337          610          615          620
339 Asp Thr Arg Ser Tyr Asn Cys Arg Val Ala Glu Ser Thr Tyr Gln His
340 625          630          635          640
342 His Pro Lys Arg Pro Ser Arg Gln Ile His Lys Gly Asp Ile Thr Leu
343          645          650          655
345 Val Pro Thr Ile Asn Gly Thr Leu Pro Ile Arg Ser His His Arg Ser
346          660          665          670
348 Ser Pro Ser Ser Ser Pro Thr Leu Glu Arg Gly Gln Met Gly Ser Arg
349          675          680          685
351 Ser Ser Asn His Val Pro Glu Asn Phe Ser Leu Glu Leu Thr His Ala
352          690          695          700
354 Thr Pro Ala Val Glu Gln Val Ser Gln Leu Leu Ser Met Leu His Gln
355 705          710          715          720
357 Gly Gln Tyr Gln Pro Arg Pro Ser Phe Arg Gly Asn Lys Tyr Ser Arg
358          725          730          735
360 Ser Tyr Arg Tyr Ala Leu Gln Asp Met Asp Lys Phe Ser Leu Lys Asp
361          740          745          750
363 Ser Gly Arg Gly Asp Ser Glu Ala Gly Asp Ser Asp Tyr Asp Leu Gly
364          755          760          765
366 Arg Asp Ser Pro Ile Asp Arg Leu Leu Gly Glu Gly Phe Ser Asp Leu
367          770          775          780

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 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

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455 Val Tyr Ser Phe Ser Ser His Val Ser Pro Lys Ile Met Glu Thr Phe
456 225                      230                      235                      240
458 Asp Tyr Glu Ile Thr Lys Ser Tyr Glu Ile Asp Val Gln Ala Gln Asp
459                      245                      250                      255
461 Leu Gly Pro Asn Ser Ile Pro Ala His Cys Lys Ile Ile Ile Lys Val
462                      260                      265                      270
464 Val Asp Val Asn Asp Asn Lys Pro Glu Ile Asn Ile Asn Leu Met Ser
465                      275                      280                      285
467 Pro Gly Lys Glu Glu Ile Ser Tyr Ile Phe Glu Gly Asp Pro Ile Asp
468                      290                      295                      300
470 Thr Phe Val Ala Leu Val Arg Val Gln Asp Lys Asp Ser Gly Leu Asn
471 305                      310                      315                      320
473 Gln Lys Thr Tyr Glu Asn Asn Tyr Leu Ile Leu Thr Asn Ala Thr Leu
474                      325                      330                      335
476 Asp Arg Glu Lys Arg Ser Glu Tyr Ser Leu Thr Val Ile Ala Glu Asp
477                      340                      345                      350
479 Arg Gly Thr Pro Ser Leu Ser Thr Val Lys His Phe Thr Val Gln Ile
480                      355                      360                      365
482 Asn Asp Ile Asn Asp Asn Pro Pro His Phe Gln Arg Ser Arg Tyr Glu
483                      370                      375                      380
485 Phe Val Ile Ser Glu Asn Asn Ser Pro Gly Ala Tyr Ile Thr Thr Val
486 385                      390                      395                      400
488 Thr Ala Thr Asp Pro Asp Leu Gly Glu Asn Gly Gln Val Thr Tyr Thr
489                      405                      410                      415
491 Thr Ile Asp Pro Ser Asn Gly Ala Ile Tyr Ala Leu Arg Ile Phe Asp
492                      420                      425                      430
494 His Glu Glu Val Ser Gln Ile Thr Phe Val Val Glu Ala Arg Asp Gly
495                      435                      440                      445
497 Gly Ser Pro Lys Lys Gln Leu Val Ser Asn Thr Thr Val Val Leu Thr Ile
498                      450                      455                      460
500 Ile Asp Glu Asn Asp Asn Val Pro Val Val Ile Gly Pro Ala Leu Arg
501 465                      470                      475                      480
503 Asn Asn Thr Ala Glu Ile Thr Ile Pro Lys Gly Ala Glu Ser Gly Phe
504                      485                      490                      495
506 Ala Glu Leu Ser Cys Ala Ile Val Ala Gly Asn Glu Glu Asn Ile Phe
507                      500                      505                      510
509 Ile Ile Asp Pro Arg Ser Cys Asp Ile His Thr Asn Val Ser Met Asp
510                      515                      520                      525
512 Ser Val Pro Tyr Thr Glu Trp Glu Leu Ser Val Ile Ile Gln Asp Lys
513                      530                      535                      540
515 Gly Asn Pro Gln Leu His Thr Lys Val Leu Leu Lys Cys Met Ile Phe
516 545                      550                      555                      560
518 Glu Tyr Ala Glu Ser Val Thr Ser Thr Ala Met Thr Ser Val Ser Gln
519                      565                      570                      575
521 Ile Cys Ala Val Leu Leu Val Ile Met Val Leu Phe Ala Thr Arg Cys
522                      580                      585                      590
524 Asn Arg Glu Lys Lys Asp Thr Arg Ser Tyr Asn Cys Arg Val Ala Glu
525                      595                      600                      605
527 Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg Gln Ile His Lys

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528      610      615      620
530 Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr Leu Pro Ile Arg
531 625      630      635      640
533 Ser His His Arg Ser Ser Pro Ser Ser Ser Pro Thr Leu Glu Arg Gly
534      645      650      655
536 Gln Met Gly Ser Arg Gln Ser His Asn Ser His Gln Ser Leu Asn Ser
537      660      665      670
539 Glu Leu Thr His Ala Thr Pro Ala Val Glu Gln Val Ser Gln Leu Leu
540      675      680      685
542 Ser Met Leu His Gln Gly Gln Tyr Gln Pro Arg Pro Ser Phe Arg Gly
543      690      695      700
545 Asn Lys Tyr Ser Arg Ser Tyr Arg Tyr Ala Leu Gln Asp Met Asp Lys
546 705      710      715      720
548 Phe Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala Gly Asp Ser
549      725      730      735
551 Asp Tyr Asp Leu Gly Arg Asp Ser Pro Ile Asp Arg Leu Leu Gly Glu
552      740      745      750
554 Met Arg Leu Cys Thr Glu Glu Cys Arg Val Leu Gly His Ser Asp Gln
555      755      760      765
557 Cys Trp Met Pro Pro Leu Pro Ser Pro Ser Ser Asp Tyr Arg Ser Asn
558      770      775      780
560 Met Phe Ile Pro Gly Glu Glu Phe Pro Thr Gln Pro Gln Gln Gln His
561 785      790      795      800
563 Pro His Gln Ser Leu Glu Asp Asp Ala Gln Pro Ala Asp Ser Gly Glu
564      805      810      815
566 Lys Lys Lys Ser Phe Ser Thr Phe Gly Lys Asp Ser Pro Asn Asp Glu
567      820      825      830
569 Ser Ser Val Phe Gln Arg Leu Leu Pro Pro Ser Leu Asp Thr Tyr Ser
570      835      840      845
572 Gly Pro Pro Leu Gly Thr His Ser Ser Val Gln Pro Ser Ser Lys Trp
573      850      855      860
575 Met Asp Ala Ser Glu Leu Val Ala Glu Ile Asn Lys Leu Leu Gln Asp
576 865      870      875      880
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583 <211> LENGTH: 679
584 <212> TYPE: PRT
585 <213> ORGANISM: Homo sapiens
587 <400> SEQUENCE: 6
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589 1 5 10 15
591 Ile Ala Arg Leu Ser Glu Asp Val Ala Asp Val Leu Leu Lys Leu Pro
592 20 25 30
594 Asn Pro Ser Thr Val Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro
595 35 40 45
597 Leu Leu Val Val Asn Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr
598 50 55 60
600 Glu Phe Asp Val Ile Thr Leu Pro Thr Glu His Leu Gln Leu Phe His
601 65 70 75 80

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679 listed
 583 found

RAW SEQUENCE LISTING

DATE: 01/29/2001

PATENT APPLICATION: US/09/759,130

TIME: 13:45:10

Input Set : A:\10147-61.txt

Output Set: N:\CRF3\01292001\I759130.raw

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604                               85                               90                               95
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607                               100                              105                              110
609 Arg Ile Pro Leu Asp Ser Ala Phe Asp Pro Asp Val Gly Glu Asn Ser
610                               115                              120                              125
612 Leu His Thr Tyr Ser Leu Ser Ala Asn Asp Phe Phe Asn Ile Glu Val
613                               130                              135                              140
615 Arg Thr Arg Thr Asp Gly Ala Lys Tyr Ala Glu Leu Ile Val Val Arg
616 145                               150                              155                              160
618 Ala Ser Asp Met Gly Val Pro Gln Arg Ser Gly Ser Ser Ile Leu Lys
619                               165                              170                              175
621 Ile Ser Ile Ser Asp Ser Asn Asp Asn Ser Pro Ala Phe Glu Gln Gln
622                               180                              185                              190
624 Ser Tyr Ile Ile Gln Leu Leu Glu Asn Ser Pro Val Gly Thr Leu Leu
625                               195                              200                              205
627 Leu Asp Leu Asn Ala Thr Asp Pro Asp Glu Gly Ala Asn Gly Lys Ile
628                               210                              215                              220
630 Val Tyr Ser Phe Ser Ser His Val Ser Pro Lys Ile Met Glu Thr Phe
631 225                               230                              235                              240
633 Asp Tyr Glu Ile Thr Lys Ser Tyr Glu Ile Asp Val Gln Ala Gln Asp
634                               245                              250                              255
636 Leu Gly Pro Asn Ser Ile Pro Ala His Cys Lys Ile Ile Ile Lys Val
637                               260                              265                              270
639 Val Asp Val Asn Asp Asn Lys Pro Glu Ile Asn Ile Asn Leu Met Ser
640                               275                              280                              285
642 Pro Gly Lys Glu Glu Ile Ser Tyr Ile Phe Glu Gly Asp Pro Ile Asp
643                               290                              295                              300
645 Thr Phe Val Ala Leu Val Arg Val Gln Asp Lys Asp Ser Gly Leu Asn
646 305                               310                              315                              320
648 Gln Lys Thr Tyr Glu Asn Asn Tyr Leu Ile Leu Thr Asn Ala Thr Leu
649                               325                              330                              335
651 Asp Arg Glu Lys Arg Ser Glu Tyr Ser Leu Thr Val Ile Ala Glu Asp
652                               340                              345                              350
654 Arg Gly Thr Pro Ser Leu Ser Thr Val Lys His Phe Thr Val Gln Ile
655                               355                              360                              365
657 Asn Asp Ile Asn Asp Asn Pro Pro His Phe Gln Arg Ser Arg Tyr Glu
658                               370                              375                              380
660 Phe Val Ile Ser Glu Asn Asn Ser Pro Gly Ala Tyr Ile Thr Thr Val
661 385                               390                              395                              400
663 Thr Ala Thr Asp Pro Asp Leu Gly Glu Asn Gly Gln Val Thr Tyr Thr
664                               405                              410                              415
666 Thr Ile Asp Pro Ser Asn Gly Ala Ile Tyr Ala Leu Arg Ile Phe Asp
667                               420                              425                              430
669 His Glu Glu Val Ser Gln Ile Thr Phe Val Val Glu Ala Arg Asp Gly
670                               435                              440                              445
672 Gly Ser Pro Lys Gln Leu Val Ser Asn Thr Thr Val Val Leu Thr Ile
673                               450                              455                              460
675 Ile Asp Glu Asn Asp Asn Val Pro Val Val Ile Gly Pro Ala Leu Arg

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 PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
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Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\1759130.raw

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676 465          470          475          480
678 Asn Asn Thr Ala Glu Ile Thr Ile Pro Lys Gly Ala Glu Ser Gly Phe
679          485          490          495
681 Ala Glu Leu Ser Cys Ala Ile Val Ala Gly Asn Glu Glu Asn Ile Phe
682          500          505          510
684 Ile Ile Asp Pro Arg Ser Cys Asp Ile His Thr Asn Val Ser Met Asp
685          515          520          525
687 Ser Val Pro Tyr Thr Glu Trp Glu Leu Ser Val Ile Ile Gln Asp Lys
688          530          535          540
690 Gly Asn Pro Gln Leu His Thr Lys Val Leu Leu Lys Cys Met Ile Phe
691 545          550          555          560
693 Glu Tyr Ala Glu Ser Val Thr Ser Thr Ala Met Thr Ser Val Ser Gln
694          565          570          575
696 Ala Ser Leu Asp Val Ser Met
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701 <211> LENGTH: 22
702 <212> TYPE: PRT
703 <213> ORGANISM: Homo sapiens
705 <400> SEQUENCE: 7
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E--> 707 1          50          10          15
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713 <213> ORGANISM: Homo sapiens
715 <400> SEQUENCE: 8
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719 Val Ala Glu Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg Gln
720          20          25          30
722 Ile His Lys Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr Leu
723          35          40          45
725 Pro Ile Arg Ser His His Arg Ser Ser Pro Ser Ser Pro Thr Leu
726          50          55          60
728 Glu Arg Gly Gln Met Gly Ser Arg Gln Ser His Asn Ser His Gln Ser
729 65          70          75          80
731 Phe Ser Leu Glu Leu Thr His Ala Thr Pro Ala Val Glu Gln Val Ser
732          85          90          95
734 Gln Leu Leu Ser Met Leu His Gln Gly Gln Tyr Gln Pro Arg Pro Ser
735          100          105          110
737 Phe Arg Gly Asn Lys Tyr Ser Arg Ser Tyr Arg Tyr Ala Leu Gln Asp
738          115          120          125
740 Met Asp Lys Phe Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala
741          130          135          140
743 Gly Asp Ser Asp Tyr Asp Leu Gly Arg Asp Ser Pro Ile Asp Arg Leu
744 145          150          155          160
746 Pro Ala Ala Met Arg Leu Cys Thr Glu Glu Cys Arg Val Leu Gly His
747          165          170          175

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- 583 shown
 679 listed seq. #6

Delete this

- 22 listed
 - 16 found

- 423 listed
 - 295 shown

RAW SEQUENCE LISTING

DATE: 01/29/2001

PATENT APPLICATION: US/09/759,130

TIME: 13:45:10

Input Set : A:\10147-61.txt

Output Set: N:\CRF3\01292001\I759130.raw

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749 Ser Asp Gln Cys Trp Met Pro Pro Leu Pro Ser Pro Ser Ser Asp Tyr
750      180      185      190
752 Arg Ser Asn Met Phe Ile Pro Gly Glu Glu Phe Pro Thr Gln Pro Gln
753      195      200      205
755 Gln Gln His Pro His Gln Ser Leu Glu Asp Asp Ala Gln Pro Ala Asp
756      210      215      220
758 Ser Gly Glu Lys Lys Lys Ser Phe Ser Thr Phe Gly Lys Asp Ser Pro
759 225      230      235      240
761 Ser Glu Met Ser Ser Val Phe Gln Arg Leu Leu Pro Pro Ser Leu Asp
762      245      250      255
764 Thr Asn Cys Gly Pro Pro Leu Gly Thr His Ser Ser Val Gln Pro Ser
765      260      265      270
767 His Glu Leu Met Asp Ala Ser Glu Leu Val Ala Glu Ile Asn Lys Leu
768      275      280      285
770 Leu Gln Asp Val Arg Gln Ser
E--> 771      290      295
1043 <210> SEQ ID NO: 33
1044 <211> LENGTH: 1150
1045 <212> TYPE: PRT
1046 <213> ORGANISM: Homo sapiens
1048 <400> SEQUENCE: 33
1049 Met His Gln Met Asn Ala Lys Met His Phe Arg Phe Val Phe Ala Leu
1050      1      5      10      15
1052 Leu Ile Val Ser Phe Asn His Asp Val Leu Gly Lys Asn Leu Lys Tyr
1053      20      25      30
1055 Arg Ile Tyr Glu Glu Gln Arg Val Gly Ser Val Ile Ala Arg Leu Ser
1056      35      40      45
1058 Glu Asp Val Ala Asp Val Leu Lys Leu Pro Asn Pro Ser Thr Val
1059      50      55      60
1061 Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro Leu Leu Val Val Asn
1062      65      70      75      80
1064 Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr Ile Asp Arg Glu Gln
1065      85      90      95
1067 Thr Leu Pro Thr Glu His Leu Gln Leu Phe His Ile Glu Val Glu Val
1068      100     105     110
1070 Leu Asp Ile Asn Asp Asn Ser Pro Gln Phe Ser Arg Ser Leu Ile Pro
1071      115     120     125
1073 Ile Glu Ile Ser Glu Ser Ala Ala Val Gly Thr Arg Ile Pro Leu Asp
1074      130     135     140
1076 Ser Ala Phe Asp Pro Asp Val Gly Glu Asn Ser Leu His Thr Tyr Ser
1077 145      150      155      160
1079 Leu Ser Ala Asn Asp Phe Phe Asn Ile Glu Val Arg Thr Arg Thr Asp
1080      165     170     175
1082 Glu Leu Lys Ser Ser Tyr Glu Leu Gln Leu Thr Ala Ser Asp Met Gly
1083      180     185     190
1085 Val Pro Gln Arg Ser Gly Ser Ser Ile Leu Lys Ile Ser Ile Ser Asp
1086      195     200     205
1088 Ser Asn Asp Asn Ser Pro Ala Phe Glu Gln Gln Ser Tyr Ile Ile Gln
1089      210     215     220

```

295 shown, 423 listed

1150 listed, 910 shown

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

```

1091 Leu Leu Glu Asn Ser Pro Val Gly Thr Leu Leu Leu Asp Leu Asn Ala
1092 225 230 235 240
1094 Thr Asp Pro Asp Glu Gly Ala Asn Gly Lys Ile Val Tyr Ser Phe Ser
1095 245 250 255
1097 Ser His Val Ser Pro Lys Ile Met Glu Thr Phe Lys Ile Asp Ser Glu
1098 260 265 270
1100 Lys Ser Tyr Glu Ile Asp Val Gln Ala Gln Asp Leu Gly Pro Asn Ser
1101 275 280 285
1103 Ile Pro Ala His Cys Lys Ile Ile Ile Lys Val Val Asp Val Asn Asp
1104 290 295 300
1106 Asn Lys Pro Glu Ile Asn Ile Asn Leu Met Ser Pro Gly Lys Glu Glu
1107 305 310 315 320
1109 Ile Ser Tyr Ile Phe Glu Gly Asp Pro Ile Asp Thr Phe Val Ala Leu
1110 325 330 335
1112 Val Arg Val Gln Asp Lys Asp Ser Gly Leu Asn Gly Glu Ile Val Cys
1113 340 345 350
1115 Asn Asn Tyr Leu Ile Leu Thr Asn Ala Thr Leu Asp Arg Glu Lys Arg
1116 355 360 365
1118 Ser Glu Tyr Ser Leu Thr Val Ile Ala Glu Asp Arg Gly Thr Pro Ser
1119 370 375 380
1121 Leu Ser Thr Val Lys His Phe Thr Val Gln Ile Asn Asp Ile Asn Asp
1122 385 390 395 400
1124 Asn Pro Pro His Phe Gln Arg Ser Arg Tyr Glu Phe Val Ile Ser Glu
1125 405 410 415
1127 Asn Asn Ser Pro Gly Ala Tyr Ile Thr Thr Val Thr Ala Thr Asp Pro
1128 420 425 430
1130 Phe Ile Leu Gly Ser Ser Ile Thr Thr Tyr Val Thr Ile Asp Pro Ser
1131 435 440 445
1133 Asn Gly Ala Ile Tyr Ala Leu Arg Ile Phe Asp His Glu Glu Val Ser
1134 450 455 460
1136 Gln Ile Thr Phe Val Val Glu Ala Arg Asp Gly Gly Ser Pro Lys Gln
1137 465 470 475 480
1139 Leu Val Ser Asn Thr Thr Val Val Leu Thr Ile Ile Asp Glu Asn Asp
1140 485 490 495
1142 Asn Val Pro Val Val Ile Gly Pro Ala Leu Arg Asn Asn Thr Ala Glu
1143 500 505 510
1145 Ile Thr Ile Pro Lys Gly Ala Glu Ser Gly Phe His Val Thr Arg Ile
1146 515 520 525
1148 Ala Ile Val Ala Gly Asn Glu Asn Ile Phe Ile Ile Asp Pro Arg
1149 530 535 540
1151 Ser Cys Asp Ile His Thr Asn Val Ser Met Asp Ser Val Pro Tyr Thr
1152 545 550 555 560
1154 Glu Trp Glu Leu Ser Val Ile Ile Gln Asp Lys Gly Asn Pro Gln Leu
1155 565 570 575
1157 His Thr Lys Val Leu Leu Lys Cys Met Ile Phe Glu Tyr Ala Glu Ser
1158 580 585 590
1160 Val Thr Ser Thr Ala Met Thr Ser Val Ser Gln Ala Ser Leu Asp Val
1161 595 600 605
1163 Leu Val Ile Met Val Leu Phe Ala Thr Arg Cys Asn Arg Glu Lys Lys

```

RAW SEQUENCE LISTING

DATE: 01/29/2001

PATENT APPLICATION: US/09/759,130

TIME: 13:45:10

Input Set : A:\10147-61.txt

Output Set: N:\CRF3\01292001\I759130.raw

```

1164      610      615      620
1166 Asp Thr Arg Ser Tyr Asn Cys Arg Val Ala Glu Ser Thr Tyr Gln His
1167 625      630      635      640
1169 His Pro Lys Arg Pro Ser Arg Gln Ile His Lys Gly Asp Ile Thr Leu
1170      645      650      655
1172 Val Pro Thr Ile Asn Gly Thr Leu Pro Ile Arg Ser His His Arg Ser
1173      660      665      670
1175 Ser Pro Ser Ser Ser Pro Thr Leu Glu Arg Gly Gln Met Gly Ser Arg
1176      675      680      685
1178 Ser Ser Asn His Val Pro Glu Asn Phe Ser Leu Glu Leu Thr His Ala
1179      690      695      700
1181 Thr Pro Ala Val Glu Val Ser Gln Leu Leu Ser Met Leu His Gln Gly
1182 705      710      715      720
1184 Gln Tyr Gln Pro Arg Pro Ser Phe Arg Gly Asn Lys Tyr Ser Arg Ser
1185      725      730      735
1187 Tyr Arg Tyr Ala Leu Gln Asp Met Asp Lys Phe Ser Leu Lys Asp Ser
1188      740      745      750
1190 Gly Arg Gly Asp Ser Glu Ala Gly Asp Ser Asp Tyr Asp Leu Gly Arg
1191      755      760      765
1193 Asp Ser Pro Ile Asp Arg Leu Leu Gly Glu Gly Phe Ser Asp Leu Phe
1194      770      775      780
1196 Glu Cys Arg Val Leu Gly His Ser Asp Gln Cys Trp Met Pro Pro Leu
1197 785      790      795      800
1199 Pro Ser Pro Ser Ser Asp Tyr Arg Ser Asn Met Phe Ile Pro Gly Glu
1200      805      810      815
1202 Glu Phe Pro Thr Gln Pro Gln Gln Gln His Pro His Gln Ser Leu Glu
1203      820      825      830
1205 Asp Asp Ala Gln Pro Ala Asp Ser Gly Glu Lys Lys Lys Ser Phe Ser
1206      835      840      845
1208 Thr Phe Gly Lys Asp Ser Pro Asn Asp Glu Asp Thr Gly Asp Thr Ser
1209      850      855      860
1211 Asp Arg Ser Asn Ser Leu Glu Arg Arg Lys Gly Pro Leu Pro Ala Lys
1212 865      870      875      880
1214 Asn His Leu Asn Asp Gly Lys His Glu Leu Met Asp Ala Ser Glu Leu
1215      885      890      895
1217 Val Ala Glu Ile Asn Lys Leu Leu Gln Asp Val Arg Gln Ser
E--> 1218      900      905      910
1226 <210> SEQ ID NO: 35
1227 <211> LENGTH: 1123
1228 <212> TYPE: PRT
1229 <213> ORGANISM: Homo sapiens
1231 <400> SEQUENCE: 35
1232 Lys Asn Leu Lys Tyr Arg Ile Tyr Glu Glu Gln Arg Val Gly Ser Val
1233 1 5 10 15
1235 Ile Ala Arg Leu Ser Glu Asp Val Ala Asp Val Leu Leu Lys Leu Pro
1236 20 25 30
1238 Asn Pro Ser Thr Val Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro
1239 35 40 45
1241 Leu Leu Val Val Asn Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr

```

1150 listed
910 shown
seq # 33

1123 listed, 883 shown

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

```

1242      50      55      60
1244 Glu Phe Asp Val Ile Thr Leu Pro Thr Glu His Leu Gln Leu Phe His
1245 65      70      75      80
1247 Ile Glu Val Glu Val Leu Asp Ile Asn Asp Asn Ser Pro Gln Phe Ser
1248      85      90      95
1250 Arg Ser Leu Ile Pro Ile Glu Ile Ser Glu Ser Ala Ala Val Gly Thr
1251      100      105      110
1253 Arg Ile Pro Leu Asp Ser Ala Phe Asp Pro Asp Val Gly Glu Asn Ser
1254      115      120      125
1256 Leu His Thr Tyr Ser Leu Ser Ala Asn Asp Phe Phe Asn Ile Glu Val
1257      130      135      140
1259 Arg Thr Arg Thr Asp Gly Ala Lys Tyr Ala Glu Leu Ile Val Val Arg
1260 145      150      155      160
1262 Ala Ser Asp Met Gly Val Pro Gln Arg Ser Gly Ser Ser Ile Leu Lys
1263      165      170      175
1265 Ile Ser Ile Ser Asp Ser Asn Asp Asn Ser Pro Ala Phe Glu Gln Gln
1266      180      185      190
1268 Ser Tyr Ile Ile Gln Leu Leu Glu Asn Ser Pro Val Gly Thr Leu Leu
1269      195      200      205
1271 Leu Asp Leu Asn Ala Thr Asp Pro Asp Glu Gly Ala Asn Gly Lys Ile
1272      210      215      220
1274 Val Tyr Ser Phe Ser Ser His Val Ser Pro Lys Ile Met Glu Thr Phe
1275 225      230      235      240
1277 Asp Tyr Glu Ile Thr Lys Ser Tyr Glu Ile Asp Val Gln Ala Gln Asp
1278      245      250      255
1280 Leu Gly Pro Asn Ser Ile Pro Ala His Cys Lys Ile Ile Ile Lys Val
1281      260      265      270
1283 Val Asp Val Asn Asp Asn Lys Pro Glu Ile Asn Ile Asn Leu Met Ser
1284      275      280      285
1286 Pro Gly Lys Glu Glu Ile Ser Tyr Ile Phe Glu Gly Asp Pro Ile Asp
1287      290      295      300
1289 Thr Phe Val Ala Leu Val Arg Val Gln Asp Lys Asp Ser Gly Leu Asn
1290 305      310      315      320
1292 Gln Lys Thr Tyr Glu Asn Asn Tyr Leu Ile Leu Thr Asn Ala Thr Leu
1293      325      330      335
1295 Asp Arg Glu Lys Arg Ser Glu Tyr Ser Leu Thr Val Ile Ala Glu Asp
1296      340      345      350
1298 Arg Gly Thr Pro Ser Leu Ser Thr Val Lys His Phe Thr Val Gln Ile
1299      355      360      365
1301 Asn Asp Ile Asn Asp Asn Pro Pro His Phe Gln Arg Ser Arg Tyr Glu
1302      370      375      380
1304 Phe Val Ile Ser Glu Asn Asn Ser Pro Gly Ala Tyr Ile Thr Thr Val
1305 385      390      395      400
1307 Thr Ala Thr Asp Pro Asp Leu Gly Glu Asn Gly Gln Val Thr Tyr Thr
1308      405      410      415
1310 Thr Ile Asp Pro Ser Asn Gly Ala Ile Tyr Ala Leu Arg Ile Phe Asp
1311      420      425      430
1313 His Glu Glu Val Ser Gln Ile Thr Phe Val Val Glu Ala Arg Asp Gly
1314      435      440      445

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001

TIME: 13:45:10

Input Set : A:\10147-61.txt

Output Set: N:\CRF3\01292001\I759130.raw

```

1316 Gly Ser Pro Lys Gln Leu Val Ser Asn Thr Thr Val Val Leu Thr Ile
1317      450      455      460
1319 Ile Asp Glu Asn Asp Asn Val Pro Val Val Ile Gly Pro Ala Leu Arg
1320 465      470      475      480
1322 Asn Asn Thr Ala Glu Ile Thr Ile Pro Lys Gly Ala Glu Ser Gly Phe
1323      485      490      495
1325 Ala Glu Leu Ser Cys Ala Ile Val Ala Gly Asn Glu Glu Asn Ile Phe
1326      500      505      510
1328 Ile Ile Asp Pro Arg Ser Cys Asp Ile His Thr Asn Val Ser Met Asp
1329      515      520      525
1331 Ser Val Pro Tyr Thr Glu Trp Glu Leu Ser Val Ile Ile Gln Asp Lys
1332      530      535      540
1334 Gly Asn Pro Gln Leu His Thr Lys Val Leu Leu Lys Cys Met Ile Phe
1335 545      550      555      560
1337 Glu Tyr Ala Glu Ser Val Thr Ser Thr Ala Met Thr Ser Val Ser Gln
1338      565      570      575
1340 Ile Cys Ala Val Leu Leu Val Ile Met Val Leu Phe Ala Thr Arg Cys
1341      580      585      590
1343 Asn Arg Glu Lys Lys Asp Thr Arg Ser Tyr Asn Cys Arg Val Ala Glu
1344      595      600      605
1346 Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg Gln Ile His Lys
1347      610      615      620
1349 Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr Leu Pro Ile Arg
1350 625      630      635      640
1352 Ser His His Arg Ser Ser Pro Ser Ser Ser Pro Thr Leu Glu Arg Gly
1353      645      650      655
1355 Gln Met Gly Ser Arg Gln Ser His Asn Ser His Gln Ser Leu Asn Ser
1356      660      665      670
1358 Glu Leu Thr His Ala Thr Pro Ala Val Glu Val Ser Gln Leu Leu Ser
1359      675      680      685
1361 Met Leu His Gln Gly Gln Tyr Gln Pro Arg Pro Ser Phe Arg Gly Asn
1362      690      695      700
1364 Lys Tyr Ser Arg Ser Tyr Arg Tyr Ala Leu Gln Asp Met Asp Lys Phe
1365 705      710      715      720
1367 Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala Gly Asp Ser Asp
1368      725      730      735
1370 Tyr Asp Leu Gly Arg Asp Ser Pro Ile Asp Arg Leu Leu Gly Glu Gly
1371      740      745      750
1373 Arg Leu Cys Thr Glu Glu Cys Arg Val Leu Gly His Ser Asp Gln Cys
1374      755      760      765
1376 Trp Met Pro Pro Leu Pro Ser Pro Ser Ser Asp Tyr Arg Ser Asn Met
1377      770      775      780
1379 Phe Ile Pro Gly Glu Glu Phe Pro Thr Gln Pro Gln Gln Gln His Pro
1380 785      790      795      800
1382 His Gln Ser Leu Glu Asp Asp Ala Gln Pro Ala Asp Ser Gly Glu Lys
1383      805      810      815
1385 Lys Lys Ser Phe Ser Thr Phe Gly Lys Asp Ser Pro Asn Asp Glu Asp
1386      820      825      830
1388 Ser Val Phe Gln Arg Leu Leu Pro Pro Ser Leu Asp Thr Tyr Ser Glu

```

RAW SEQUENCE LISTING

DATE: 01/29/2001

PATENT APPLICATION: US/09/759,130

TIME: 13:45:10

Input Set : A:\10147-61.txt

Output Set: N:\CRF3\01292001\I759130.raw

```

1389      835      840      845
1391 Leu Pro Ala Met Glu Glu Ile Pro Glu Asn Tyr Glu Glu Asp Asp Phe
1392      850      855      860
1394 Asp Ala Ser Glu Leu Val Ala Glu Ile Asn Lys Leu Leu Gln Asp Val
1395 865      870      875      880
E--> 1397 Arg Gln Ser 883
1411 <210> SEQ ID NO: 38
1412 <211> LENGTH 423
1413 <212> TYPE: PRT
1414 <213> ORGANISM: Homo sapiens
1416 <400> SEQUENCE: 38
1417 Ala Thr Arg Cys Asn Arg Glu Lys Lys Asp Thr Arg Ser Tyr Asn Cys
1418 1 5 10 15
1420 Arg Val Ala Glu Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg
1421 20 25 30
1423 Gln Ile His Lys Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr
1424 35 40 45
1426 Leu Pro Ile Arg Ser His His Arg Ser Ser Pro Ser Ser Pro Thr
1427 50 55 60
1429 Leu Glu Arg Gly Gln Met Gly Ser Arg Gln Ser His Asn Ser His Gln
1430 65 70 75 80
1432 Asn Phe Ser Leu Glu Thr His Ala Thr Pro Ala Val Glu Val Ser
1433 85 90 95
1435 Gln Leu Leu Ser Met Leu His Gln Gly Gln Tyr Gln Pro Arg Pro Ser
1436 100 105 110
1438 Phe Arg Gly Asn Lys Tyr Ser Arg Ser Tyr Arg Tyr Ala Leu Gln Asp
1439 115 120 125
1441 Met Asp Lys Phe Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala
1442 130 135 140
1444 Gly Asp Ser Asp Tyr Asp Leu Gly Arg Asp Ser Pro Ile Asp Arg Leu
1445 145 150 155 160
1447 Pro Ala Ala Met Arg Leu Cys Thr Glu Glu Cys Arg Val Leu Gly His
1448 165 170 175
1450 Ser Asp Gln Cys Trp Met Pro Pro Leu Pro Ser Pro Ser Ser Asp Tyr
1451 180 185 190
1453 Arg Ser Asn Met Phe Ile Pro Gly Glu Glu Phe Pro Thr Gln Pro Gln
1454 195 200 205
1456 Gln Gln His Pro His Gln Ser Leu Glu Asp Asp Ala Gln Pro Ala Asp
1457 210 215 220
1459 Ser Gly Glu Lys Lys Lys Ser Phe Ser Thr Phe Gly Lys Asp Ser Pro
1460 225 230 235 240
1462 Ser Glu Met Ser Ser Val Phe Gln Arg Leu Leu Pro Pro Ser Leu Asp
1463 245 250 255
1465 Thr Asn Cys Gly Pro Pro Leu Gly Thr His Ser Ser Val Gln Pro Ser
1466 260 265 270
1468 His Glu Leu Met Asp Ala Ser Glu Leu Val Ala Glu Ile Asn Lys Leu
1469 275 280 285
1471 Leu Gln Asp Val Arg Gln Ser
E--> 1472 290 295

```

423 listed, 295 shown

295

RAW SEQUENCE LISTING

DATE: 01/29/2001

PATENT APPLICATION: US/09/759,130

TIME: 13:45:10

Input Set : A:\10147-61.txt

Output Set: N:\CRF3\01292001\I759130.raw

1594 <210> SEQ ID NO: 42
 1595 <211> LENGTH: 1183 *1183 listed, 1135 shown*
 1596 <212> TYPE: PRT
 1597 <213> ORGANISM: Mus sp.
 1599 <400> SEQUENCE: 42

1600	Met	Met	Leu	Leu	Leu	Pro	Phe	Leu	Leu	Gly	Leu	Leu	Gly	Pro	Gly	Ser
1601	1				5					10					15	
1603	Tyr	Leu	Phe	Ile	Ser	Gly	Asp	Cys	Gln	Glu	Val	Ala	Thr	Val	Met	Val
1604				20					25					30		
1606	Lys	Phe	Gln	Val	Thr	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	Ile	Gly	Lys
1607			35					40					45			
1609	Asp	Ala	Phe	Gln	Ile	Leu	Gln	Leu	Pro	Gln	Ala	Leu	Pro	Val	Gln	Met
1610		50					55					60				
1612	Asn	Ser	Glu	Asp	Gly	Leu	Leu	Ser	Thr	Ser	Ser	Arg	Leu	Asp	Arg	Glu
1613	65					70					75				80	
1615	Lys	Leu	Cys	Arg	Gln	Glu	Asp	Pro	Cys	Leu	Val	Ser	Phe	Asp	Val	Leu
1616					85					90					95	
1618	Ala	Thr	Gly	Ala	Ser	Ala	Leu	Ile	His	Val	Glu	Ile	Gln	Val	Leu	Asp
1619			100						105					110		
1621	Ile	Asn	Asp	His	Gln	Pro	Gln	Phe	Pro	Lys	Asp	Glu	Gln	Glu	Leu	Glu
1622			115					120					125			
1624	Ile	Ser	Glu	Ser	Ala	Ser	Leu	His	Thr	Arg	Ile	Pro	Leu	Asp	Arg	Ala
1625		130					135					140				
1627	Leu	Asp	Gln	Asp	Thr	Gly	Pro	Asn	Ser	Leu	Tyr	Ser	Tyr	Ser	Leu	Ser
1628	145					150					155				160	
1630	Pro	Ser	Glu	His	Phe	Ala	Leu	Asp	Val	Ile	Val	Gly	Pro	Asp	Glu	Thr
1631					165					170					175	
1633	Lys	His	Ala	Glu	Leu	Val	Val	Val	Lys	Glu	Leu	Asp	Arg	Glu	Leu	His
1634				180					185					190		
1636	Ser	Tyr	Phe	Asp	Leu	Val	Leu	Thr	Ala	Tyr	Asp	Asn	Gly	Asn	Pro	Pro
1637			195					200					205			
1639	Lys	Ser	Gly	Ile	Ser	Val	Val	Lys	Val	Asn	Val	Leu	Asp	Ser	Asn	Asp
1640		210					215						220			
1642	Asn	Ser	Pro	Val	Phe	Ala	Glu	Ser	Ser	Leu	Ala	Leu	Glu	Ile	Pro	Glu
1643	225					230					235				240	
1645	Asp	Thr	Val	Pro	Gly	Thr	Leu	Leu	Ile	Asn	Leu	Thr	Ala	Thr	Asp	Pro
1646					245					250					255	
1648	Asp	Gln	Gly	Pro	Asn	Gly	Glu	Val	Glu	Phe	Phe	Phe	Gly	Lys	His	Val
1649				260					265					270		
1651	Ser	Pro	Glu	Val	Met	Asn	Thr	Phe	Gly	Ile	Asp	Ala	Lys	Thr	Gly	Gln
1652			275					280					285			
1654	Ile	Ile	Leu	Arg	Gln	Ala	Leu	Asp	Tyr	Glu	Lys	Asn	Pro	Ala	Tyr	Glu
1655		290					295					300				
1657	Val	Asp	Val	Gln	Ala	Arg	Asp	Leu	Gly	Pro	Asn	Ser	Ile	Pro	Gly	His
1658	305					310					315				320	
1660	Cys	Lys	Val	Leu	Ile	Lys	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	Pro	Ser
1661					325					330					335	
1663	Ile	Leu	Ile	Thr	Trp	Ala	Ser	Gln	Thr	Ser	Leu	Val	Ser	Glu	Asp	Leu
1664				340					345						350	

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/759,130
 DATE: 01/29/2001
 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

```

1666 Pro Arg Asp Ser Phe Ile Ala Leu Val Ser Ala Asn Asp Leu Asp Ser
1667          355          360          365
1669 Gly Asn Asn Gly Leu Val His Cys Trp Leu Asn Gln Glu Leu Gly His
1670          370          375          380
1672 Phe Arg Leu Lys Arg Thr Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn
1673 385          390          395          400
1675 Ala Thr Leu Asp Arg Glu Gln Trp Pro Ile Tyr Thr Leu Thr Val Phe
1676          405          410          415
1678 Ala Gln Asp Gln Gly Pro Gln Pro Leu Ser Ala Glu Lys Glu Leu Gln
1679          420          425          430
1681 Ile Gln Val Ser Asp Val Asn Asp Asn Ala Pro Val Phe Glu Lys Ser
1682          435          440          445
1684 Arg Tyr Glu Val Ser Thr Trp Glu Asn Asn Pro Pro Ser Leu His Leu
1685          450          455          460
1687 Ile Thr Leu Lys Ala His Asp Ala Asp Leu Gly Ser Asn Gly Lys Val
1688 465          470          475          480
1690 Ser Tyr Arg Ile Lys Asp Ser Pro Val Ser His Leu Val Ile Ile Asp
1691          485          490          495
1693 Phe Glu Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asp Tyr Glu Gln
1694          500          505          510
1696 Met Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Arg Gly Gln Pro
1697          515          520          525
1699 Gln Leu Ala Ser Ser Ile Ser Val Trp Val Ser Leu Leu Asp Ala Asn
1700          530          535          540
1702 Asp Asn Ala Pro Glu Val Ile Gln Pro Val Leu Ser Glu Gly Lys Ala
1703 545          550          555          560
1705 Thr Leu Ser Val Leu Val Asn Ala Ser Thr Gly His Leu Leu Leu Pro
1706          565          570          575
1708 Ile Glu Asn Pro Ser Gly Met Asp Pro Ala Gly Thr Gly Ile Pro Pro
1709          580          585          590
1711 Lys Ala Thr His Ser Pro Trp Ser Phe Leu Leu Leu Thr Ile Val Ala
1712          595          600          605
1714 Arg Asp Ala Asp Ser Gly Ala Asn Gly Glu Leu Phe Tyr Ser Ile Gln
1715          610          615          620
1717 Ser Gly Asn Asp Ala His Leu Phe Phe Leu Ser Pro Ser Leu Gly Gln
1718 625          630          635          640
1720 Leu Phe Ile Asn Val Thr Asn Ala Ser Ser Leu Ile Gly Ser Gln Trp
1721          645          650          655
1723 Asp Leu Gly Ile Val Val Glu Asp Gln Gly Ser Pro Ser Leu Gln Thr
1724          660          665          670
1726 Gln Val Ser Leu Lys Val Val Phe Val Thr Ser Val Asp His Leu Arg
1727          675          680          685
1729 Asp Ser Ala His Glu Pro Gly Val Leu Ser Thr Pro Ala Leu Ala Leu
1730          690          695          700
1732 Ile Cys Leu Ala Val Leu Leu Ala Ile Phe Gly Leu Leu Leu Ala Leu
1733 705          710          715          720
1735 Phe Val Ser Ile Cys Arg Thr Glu Arg Lys Asp Asn Arg Ala Tyr Asn
1736          725          730          735
1738 Cys Arg Glu Ala Glu Ser Ser Tyr Arg His Gln Pro Lys Arg Pro Gln

```

RAW SEQUENCE LISTING

DATE: 01/29/2001

PATENT APPLICATION: US/09/759,130

TIME: 13:45:10

Input Set : A:\10147-61.txt

Output Set: N:\CRF3\01292001\I759130.raw

```

1739          740          745          750
1741 Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val Leu Arg Ala
1742          755          760          765
1744 His Glu Asn Glu Thr Asp Glu Val Arg Pro Ser His Lys Asp Thr Ser
1745          770          775          780
1747 Lys Glu Thr Leu Met Glu Ala Gly Trp Asp Ser Cys Leu Glu Ala Pro
1748 785          790          795          800
1750 Phe His Leu Thr Pro Thr Leu Tyr Arg Thr Leu Arg Asn Gln Gly Asn
1751          805          810          815
1753 Gln Gly Glu Leu Ala Glu Ser Gln Glu Val Leu Gln Asp Thr Phe Asn
1754          820          825          830
1756 Phe Leu Phe Asn His Pro Arg Gln Arg Asn Ala Ser Arg Glu Asn Leu
1757          835          840          845
1759 Asn Leu Pro Glu Ser Pro Pro Ala Val Arg Gln Pro Leu Leu Arg Pro
1760          850          855          860
1762 Leu Lys Val Pro Gly Ser Pro Ile Ala Arg Ala Thr Gly Asp Gln Asp
1763 865          870          875          880
1765 Lys Glu Glu Ala Pro Gln Ser Pro Pro Ala Ser Ser Ala Thr Leu Arg
1766          885          890          895
1768 Arg Gln Arg Asn Phe Asn Gly Lys Val Ser Pro Arg Gly Glu Ser Gly
1769          900          905          910
1771 Pro His Gln Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe
1772          915          920          925
1774 Ala Glu Arg Asn Pro Val Glu Glu Pro Ala Gly Asp Ser Pro Pro Val
1775          930          935          940
1777 Gln Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln
1778 945          950          955          960
1780 Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly Gly
1781          965          970          975
1783 Ser Ser Arg Gly Thr Ile Pro Asp Thr Glu Gly Leu Val Gly Leu Lys
1784          980          985          990
1786 Pro Ser Gly Gln Ala Glu Pro Asp Leu Glu Glu Gly Pro Pro Ser Pro
1787          995          1000          1005
1789 Leu Ser Ser Leu Leu Asp Pro Asn Thr Gly Leu Ala Leu Asp Lys Leu
1790          1010          1015          1020
1792 Ser Pro Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu Thr
1793 1025          1030          1035          1040
1795 Ser Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Thr Val Gly Pro
1796          1045          1050          1055
1798 Gly Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val
1799          1060          1065          1070
1801 Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Gly Gln His Thr Val
1802          1075          1080          1085
1804 Pro Val Glu Ala Ala Ser Ala Ala Leu Arg Arg Leu Ser Val Cys Gly
1805          1090          1095          1100
1807 Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Gly Ala Ser Ala Ser Glu
1808 1105          1110          1115          1120
1810 Ala Gln Gly Arg Lys Lys Ala Ala Glu Ser Arg Leu Gly Cys Gly
E--> 1811          1125          1130          1135

```

1135 shown seq #42

RAW SEQUENCE LISTING DATE: 01/29/2001
PATENT APPLICATION: US/09/759,130 TIME: 13:45:12

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

9092 <210> SEQ ID NO: 300
9093 <211> LENGTH: 24 *24 listed, 15 shown*
9094 <212> TYPE: PRT
9095 <213> ORGANISM: Homo sapiens
9097 <400> SEQUENCE: 300
E--> 9098 Gln Met Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His
E--> 9099 *1 2 3 4 5 6 7 8 9 10 11 12 13 14 15*

Delete all but the amino acid numbering.

<210> 81
 <211> 4074
 <212> DNA
 <213> Homo sapiens

Seq. # 81

Missing mandatory <220> to <223>
 features to explain "n's" in the
 sequence. (See next page)

<400> 81
 gtgggtcgcg cccgaggtgag actgtgaaga aggaagaacg ttgcttgggc aaaaggagca 60
 tattctcagg agacggggcc cctgcctgcc acaccaagca ttaggccacc aggaagaccc 120
 ccattctgcaa gcaagcctag ccttccaggg agaaagaggc ccctgcagct ccttcatcat 180
 gaactggcac atgatcatct ctgggcttat tgtggtagt cttaaagttg ttggaatgac 240
 cttattttcta ctttattttcc cacagatttt taacaaaagt aacgatggtt tcaccaccac 300
 caggagctat ggaacagtct cacagatttt tgggagcagt tccccaagtc ccaacggctt 360
 cattaccaca aggagctatg gaacagtctg ccccaaagac tgggaatttt atcaagcaag 420
 atgttttttc ttatccactt ctgaatcatc ttggaatgaa agcaggggact ttgcaaagg 480
 aaaaggatcc acattggcaa ttgtcaacac gccagagaaa ctgaagtttc ttcaggacat 540
 aactgatgct gagaagtatt ttattggctt aatttaccat cgtgaagaga aaaggtggcg 600
 ttggatcaac aactctgtgt tcaatggcaa tgttaccat cagaatcaga atttcaactg 660
 tgcgaccatt ggcctaacaa agacatttga tgcctgcata tgtgacatca gctaccgcag 720
 gatctgtgag aagaatgcca aatgatcaca gttccctgtg acaagaacta tacttgcaac 780
 tctttttgaa tccatacagg tgcctgtggc aatgattctt ttacttacct atctgtctac 840
 cagtagcggt ccttgcccat ttgggaaact gagcttcttt cttctgcact gggggactgg 900
 atgctagcca tctccaggag acaggatcag ttttacggaa acaactcagt tagtatagag 960
 atgaggtccg cttctgtagt actgagcatt tctgactgat caaaaaggcc tagtctgttg 1020
 acagggtttg ttttatttta gcctcagagt ataccatact actagggagt aactgtagag 1080
 tgagaaatta taaacattat ttagggatta ccatggtgga agagggataa acataggtcc 1140
 tgtgacttcg tctctgttct caagggaacc ccattcacat gccctccta actccacaag 1200
 cgagggtagc agaggctctc ctcagtctga actaaggctt ggccttgggg agggctccta 1260
 gtgctgagct tggagcagca cggacagcag cattgtttat gggaatggag agaggctctg 1320
 gcaggatagg aaccttcttg gagacccctt tgaagaaaac caggcagcca agggagccaa 1380
 acacactaga tttctgttct tcagcaaagc cctgaagaga cacttaagct aaaaattccc 1440
 ttgtcatatt tctgaaactc cattataaca tatgtaactc ctttgtaacc aaaatttagg 1500
 taagcaggct tcctttgtct tgaaggtttt gagtacctgg ctgtatttgt tgagtatttt 1560
 taaaattttg gatagtctct taggcaacaa taatcacaat atattcatcc cttcagttct 1620
 ggagaaagcc tgataccagg cacagcctac tgaccccaag gagcctggca ctgattggca 1680
 tcacattgat ctagaactgg tccagccgcc gaagagtagg aaaagagaag ggctgctcag 1740
 ggaaacattg gctgggggca cggaataagc acatagtaaa aagggaacat cagggtcaaa 1800
 tggaaatcac ctgagacagg aaacaggag ttcatttggc cacactggaa gaaaggcaag 1860
 aaagaggaag acaagtcttg gagtacctg gctgttctcc aactcaca gacatcagct 1920
 atactctgct tgggtcataa gaaagagaaa agagatgcct tttgtgtttt gagtaagaat 1980
 aattaaacca taaggaagac catgtataaa actgatggaa ataatagtca ccaaagtaca 2040
 gcacatacca ttttgtgtct aataacaatg tagcacagta atgactgtac atgtcattgt 2100
 atgtatacca aacaagattg ttgtaaatca ttttttttat tacaacacta agttctgctt 2160
 ctgcattcct aggtttcatc atttttggct ccttagcatg gccacttaca attttttaac 2220
 atgagataac acatcagggtg tcagaacttg cttgaaggga attaccagaa gtaatttgtg 2280
 tttgagatgg ggtggaaatt ggaattatat tagtagccgg tggagataca agttctctga 2340
 ctgtgttggg aaaggataag tgctaccgtt gagaagggaa gaaaggctga gtctaggtgg 2400
 agaaaaatat caacagaact ctagccaaag gcaagcccca gaactcagac aacagaaagg 2460
 aaatcctaatt ctttctgttt tgagaagaga gaactgtagt tgcttcaact cctatttcat 2520
 gacagaataa ctgcaaaact ttaagatcag gaaatgtaga catctagtga tttctttagt 2580
 agacagttta atttccccc agattaggag acacttctgt gcaggttcta aaaggagccc 2640
 aatggcctgg ggtgggagtg gggagttagt agggaaatag tgggatttgg ttttaagttca 2700
 tcattgggag agttcctgga tccttgcaag cttagataaa tgtgatcttt attagatagc 2760
 agtggcatgc ttttaaaaaa aaaaggcaat gaaaatttag caagccactg aatttgagtt 2820
 ttcactttgt ttctaataat ctgtgtgaat cagtacagtt ttcttaccct ttcttggctt 2880
 taatttcctt actgataaaa tggggtagta atacctatct caaaaaatta ttgcacatat 2940
 taaataacat tcctctatgt atctcaatgg cattagacat taggagaagc attttgtgga 3000
 ggatttgaag ttgagatctt catccaagaa gtagcttttc aatttgctag aagcttaagt 3060

Also see
 #10 on the
 Error Summary
 Sheet.

```

taggcaagcc acttcatttt tcagaacttg tttactcatt tataatatgg gaataaaaaat 3120
ttgtgcaagt cagagaaggg tgccttaaaa atgttggtggc caagccacat gagatcaaag 3180
acacactttt catgacctca aatgtggggc cagcctagggt cagccaaccc ccatccaacc 3240
cttagactca cgaacaaatc cacctgagat cagcagagcc accctagatc agctgaaact 3300
ctaagcacia aaataaaaaa ttatcactgt aaaaaaaaaa aaaaaaaaaa aagtctctcg 3360
tatagcaaaa tctaactgat gcaatctcca tctggccttc atccttctcc ctttattgtc 3420
ctttcgtgta ttgttcatcc agcaaccagg atgatcttgt taaaacatta aacagattct 3480
gtcaykcttt maaaaaaaaa aaagccatga aattnnagca agccactgaa tttgagtttt 3540
cactttggtt tctaatatgc tgtgtgaatc agannagktt tcttaccctt tcttggtctt 3600
aatttcctta ctgataaaat ggggtwgtaa tacctatctc aaaaaattat tgcacatatt 3660
arataacatt cctctatgta tctcaatggc attagacatt aggagaagca ttttgtggag 3720
gatttgaggt tgagatcttc atccaagaag tagcttttca atttgstaga agcttaatgt 3780
aggcaagcca cttcattttt cagaacttgt ttactcattt ataatatggg aataaaaaatt 3840
tgtgcaagtc agagaagggg gccttaaaaa tgttggtggc aagccacatg agatcaaaga 3900
cacacttttc atgacctcaa atgtggggcc agcctagggt agccaacccc catccaaccc 3960
ttagactcac gaacaaatcc acctgagatc agcagagcca cctagatca gctgaaactc 4020
taagcaciaa aataaaaaact tatcactgta aaaaaaaaaa aaaaaaaaaa agaa 4074

```

*This error is indicated elsewhere in the
Sequence Listing.*

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 01/29/2001
PATENT APPLICATION: US/09/759,130 TIME: 13:45:14

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application Number
L:391 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1151 Found:911 SEQ:3
L:578 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1124 Found:884 SEQ:5
L:697 M:252 E: No. of Seq. differs, <211>LENGTH:Input:679 Found:583 SEQ:6
L:706 M:333 E: Wrong sequence grouping, Amino acids not in groups:
L:707 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:707 M:252 E: No. of Seq. differs, <211>LENGTH:Input:22 Found:15 SEQ:7
L:771 M:252 E: No. of Seq. differs, <211>LENGTH:Input:423 Found:295 SEQ:8
L:775 M:283 W: Missing Blank Line separator, <400> field identifier
L:776 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:780 M:283 W: Missing Blank Line separator, <400> field identifier
L:781 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:785 M:283 W: Missing Blank Line separator, <400> field identifier
L:786 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:790 M:283 W: Missing Blank Line separator, <400> field identifier
L:791 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:795 M:283 W: Missing Blank Line separator, <400> field identifier
L:796 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:800 M:283 W: Missing Blank Line separator, <400> field identifier
L:801 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:805 M:283 W: Missing Blank Line separator, <400> field identifier
L:806 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:810 M:283 W: Missing Blank Line separator, <400> field identifier
L:811 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:815 M:283 W: Missing Blank Line separator, <400> field identifier
L:816 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:820 M:283 W: Missing Blank Line separator, <400> field identifier
L:821 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:825 M:283 W: Missing Blank Line separator, <400> field identifier
L:826 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:830 M:283 W: Missing Blank Line separator, <400> field identifier
L:831 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:835 M:283 W: Missing Blank Line separator, <400> field identifier
L:836 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (21) SEQUENCE:
L:840 M:283 W: Missing Blank Line separator, <400> field identifier
L:841 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (22) SEQUENCE:
L:845 M:283 W: Missing Blank Line separator, <400> field identifier
L:846 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (23) SEQUENCE:
L:850 M:283 W: Missing Blank Line separator, <400> field identifier
L:851 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (24) SEQUENCE:
L:855 M:283 W: Missing Blank Line separator, <400> field identifier
L:856 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (25) SEQUENCE:
L:860 M:283 W: Missing Blank Line separator, <400> field identifier
L:861 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (26) SEQUENCE:
L:865 M:283 W: Missing Blank Line separator, <400> field identifier
L:866 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (27) SEQUENCE:
L:870 M:283 W: Missing Blank Line separator, <400> field identifier
L:871 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (28) SEQUENCE:

VERIFICATION SUMMARY DATE: 01/29/2001
PATENT APPLICATION: US/09/759,130 TIME: 13:45:14

Input Set : A:\10147-61.txt
Output Set : N:\CRF3\01292001\I759130.raw

L:875 M:283 W: Missing Blank Line separator, <400> field identifier
L:876 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (29) SEQUENCE:
L:880 M:283 W: Missing Blank Line separator, <400> field identifier
L:881 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (30) SEQUENCE:
L:1218 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1150 Found:910 SEQ:33
L:1222 M:283 W: Missing Blank Line separator, <400> field identifier
L:1223 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (34) SEQUENCE:
L:1397 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1123 Found:883 SEQ:35
L:1402 M:283 W: Missing Blank Line separator, <400> field identifier
L:1403 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (36) SEQUENCE:
L:1407 M:283 W: Missing Blank Line separator, <400> field identifier
L:1408 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (37) SEQUENCE:
L:1472 M:252 E: No. of Seq. differs, <211>LENGTH:Input:423 Found:295 SEQ:38
L:1476 M:283 W: Missing Blank Line separator, <400> field identifier
L:1477 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (39) SEQUENCE:
L:1811 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1183 Found:1135 SEQ:42
L:1815 M:283 W: Missing Blank Line separator, <400> field identifier
L:1816 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
L:1820 M:283 W: Missing Blank Line separator, <400> field identifier
L:1821 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:1825 M:283 W: Missing Blank Line separator, <400> field identifier
L:1826 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (45) SEQUENCE:
L:1830 M:283 W: Missing Blank Line separator, <400> field identifier
L:1831 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (46) SEQUENCE:
L:1835 M:283 W: Missing Blank Line separator, <400> field identifier
L:1836 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (47) SEQUENCE:
L:1840 M:283 W: Missing Blank Line separator, <400> field identifier
L:1841 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:
L:1845 M:283 W: Missing Blank Line separator, <400> field identifier
L:1846 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:
L:1850 M:283 W: Missing Blank Line separator, <400> field identifier
L:1851 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:
L:2260 M:283 W: Missing Blank Line separator, <400> field identifier
L:2261 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (62) SEQUENCE:
L:2265 M:283 W: Missing Blank Line separator, <400> field identifier
L:2266 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (63) SEQUENCE:
L:2270 M:283 W: Missing Blank Line separator, <400> field identifier
L:2271 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (64) SEQUENCE:
L:2275 M:283 W: Missing Blank Line separator, <400> field identifier
L:2276 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (65) SEQUENCE:
L:2280 M:283 W: Missing Blank Line separator, <400> field identifier
L:2281 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (66) SEQUENCE:
L:2285 M:283 W: Missing Blank Line separator, <400> field identifier
L:2286 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (67) SEQUENCE:
L:2290 M:283 W: Missing Blank Line separator, <400> field identifier
L:2291 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (68) SEQUENCE:
L:2295 M:283 W: Missing Blank Line separator, <400> field identifier
L:2296 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (69) SEQUENCE:
L:2300 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY DATE: 01/29/2001
PATENT APPLICATION: US/09/759,130 TIME: 13:45:14

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

L:2301 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (70) SEQUENCE:
L:2864 M:283 W: Missing Blank Line separator, <400> field identifier
L:2865 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (79) SEQUENCE:
L:2869 M:283 W: Missing Blank Line separator, <400> field identifier
L:2870 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (80) SEQUENCE:
L:2937 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:81
L:2937 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:81
L:2937 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:81
L:2937 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:81
L:2937 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:81
L:2938 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:81
L:2938 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:81
L:2938 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:81
L:2938 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:81
M:340 Repeated in SeqNo=81
L:3107 M:283 W: Missing Blank Line separator, <400> field identifier
L:3108 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (87) SEQUENCE:
L:3155 M:283 W: Missing Blank Line separator, <400> field identifier
L:3156 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (89) SEQUENCE:
L:3160 M:283 W: Missing Blank Line separator, <400> field identifier
L:3161 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (90) SEQUENCE:
L:3227 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91
L:3227 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91
L:3227 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91
L:3227 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91
L:3227 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:91
L:3228 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91
L:3228 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91
L:3228 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91
L:3228 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91
M:340 Repeated in SeqNo=91
L:3412 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:96
L:3412 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:96
L:3412 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:96
L:3412 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:96
L:3412 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:96
L:3413 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:96
L:3413 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:96
L:3413 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:96
L:3413 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:96
M:340 Repeated in SeqNo=96
L:3590 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:101
L:3590 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:101
L:3590 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:101
L:3590 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:101
L:3590 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:101
L:3591 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:101
L:3591 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:101
L:3591 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:101

VERIFICATION SUMMARY DATE: 01/29/2001
PATENT APPLICATION: US/09/759,130 TIME: 13:45:14

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

L:3591 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:101
M:340 Repeated in SeqNo=101
L:3764 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:106
L:3764 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:106
L:3764 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:106
L:3764 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:106
L:3764 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:106
L:3765 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:106
L:3765 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:106
L:3765 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:106
L:3765 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:106
M:340 Repeated in SeqNo=106
L:3934 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:111
L:3934 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:111
L:3934 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:111
L:3934 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:111
L:3934 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:111
L:3935 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:111
L:3935 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:111
L:3935 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:111
L:3935 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:111
M:340 Repeated in SeqNo=111
L:4037 M:283 W: Missing Blank Line separator, <400> field identifier
L:4038 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (116) SEQUENCE:
L:4042 M:283 W: Missing Blank Line separator, <400> field identifier
L:4043 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (117) SEQUENCE:
L:9098 M:333 E: Wrong sequence grouping, Amino acids not in groups!
T:9099 M:252 E: No. of Seq. differs, <211>LENGTH:Input:24 Found:15 SEQ:300
L:9617 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:324
L:9617 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:324
L:9617 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:324
L:10982 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:343
L:16673 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:450
L:16720 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:451
L:16752 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:452
L:16778 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:453
L:16805 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:454
M:340 Repeated in SeqNo=454
L:16831 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:455
L:16852 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:456
M:340 Repeated in SeqNo=456
L:16893 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:457
M:340 Repeated in SeqNo=457